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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bujard, Hermann Gossen, Manfred Salfeld, Jochen G. Voss, Jeffrey W.

- (ii) TITLE OF INVENTION: Methods for Regulating Gene Expression
- 10 (iii) NUMBER OF SEQUENCES: 10
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Lahive & Cockfield
 - (B) STREET: 60 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: ASCII text
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/383,754
 - (B) FILING DAE: 14-JUN-1994
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/076,327
 - (B) FILING DAE: 14-JUN-1993
- 35 (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: DeConti, Giulio A., Jr.
 - (B) REGISTRATION NUMBER: 31,503
 - (C) REFERENCE/DOCKET NUMBER: BBI-013CP3
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 227-7400
 - (B) TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1008 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

	(ii)	MOLE	CULE	TYP	E: D	NA (geno	mic)					
10	(vi) ((A)	INAL ORG STR	ANIS	м: н	-		mple	x Vi	rus			
	. (vii)		EDIA'				sact	ivat	or				
15	(:	ix) 1	(A)	URE: NAMI LOCA	•			08						
20	(:	ix) 1	(A)	URE : NAMI LOCA	•			08						
25	(:	ix) 1	(A)	URE: NAMI LOCA					ding					
30	(:	ix) 1	(A)	URE : NAMI LOCA					ding					
	(:	ix) 1	(A)	JRE : NAMI LOCA	•			05						
35	(2	ki) S	SEQUI	ENCE	DES	CRIP	rion	: SE	Q ID	NO:	L:			
				GAT Asp 5										48
40				GGA Gly										96
45				GAG Glu										144
50				GAC Asp										192
55				CCT Pro										240
				AGT Ser 85										288

	GCA Ala	AAA Lys	GTA Val	CAT His 100	TTA Leu	GGT Gly	ACA Thr	CGG Arg	CCT Pro 105	ACA Thr	GAA Glu	AAA Lys	CAG Gln	TAT Tyr 110	GAA Glu	ACT Thr	336
5	CTC Leu	GAA Glu	AAT Asn 115	CAA Gln	TTA Leu	GCC Ala	TTT Phe	TTA Leu 120	TGC Cys	CAA Gln	CAA Gln	GGT Gly	TTT Phe 125	TCA Ser	CTA Leu	GAG Glu	384
10	AAT Asn	GCA Ala 130	TTA Leu	TAT Tyr	GCA Ala	CTC Leu	AGC Ser 135	GCT Ala	GTG Val	GGG Gly	CAT His	TTT Phe 140	ACT Thr	TTA Leu	GGT Gly	TGC Cys	432
15	GTA Val 145	TTG Leu	GAA Glu	GAT Asp	CAA Gln	GAG Glu 150	CAT His	CAA Gln	GTC Val	GCT Ala	AAA Lys 155	GAA Glu	GAA Glu	AGG Arg	GAA Glu	ACA Thr 160	480 ·
20	CCT Pro	ACT Thr	ACT Thr	GAT Asp	AGT Ser 165	ATG Met	CCG Pro	CCA Pro	TTA Leu	TTA Leu 170	CGA Arg	CAA Gln	GCT Ala	ATC Ile	GAA Glu 175	TTA Leu	528
25	TTT Phe	GAT Asp	CAC His	CAA Gln 180	GGT Gly	GCA Ala	GAG Glu	CCA Pro	GCC Ala 185	TTC Phe	TTA Leu	TTC Phe	GGC Gly	CTT Leu 190	GAA Glu	TTG Leu	576
25	ATC Ile	ATA Ile	TGC Cys 195	GGA Gly	TTA Leu	GAA Glu	AAA Lys	CAA Gln 200	CTT Leu	AAA Lys	TGT Cys	GAA Glu	AGT Ser 205	GGG Gly	TCC Ser	GCG Ala	624
30	TAC Tyr	AGC Ser 210	Arg	GCG Ala	CGT Arg	ACG Thr	AAA Lys 215	AAC Asn	AAT Asn	TAC Tyr	GGG Gly	TCT Ser 220	ACC Thr	ATC Ile	GAG Glu	GGC Gly	672
35	CTG Leu 225	Leu	GAT Asp	CTC Leu	CCG Pro	GAC Asp 230	GAC Asp	GAC Asp	GCC Ala	CCC Pro	GAA Glu 235	Glu	GCG Ala	GGG Gly	CTG Leu	GCG Ala 240	720
40	GCT Ala	CCG	CGC Arg	CTG Leu	TCC Ser 245	Phe	Leu	Pro	GCG Ala	Gly	His	ACG Thr	CGC Arg	AGA Arg	CTG Leu 255	TCG Ser	768
45	ACG Thr	GCC Ala	CCC Pro	CCG Pro 260	Thr	GAT Asp	GTC Val	AGC Ser	CTG Leu 265	Gly	GAC Asp	GAG Glu	CTC Leu	CAC His	Let	GAC Asp	816
45	GGC	GAC Glu	G GAC 1 Asp 275	val	GCG Ala	ATG Met	GCG Ala	CAT His	Ala	GAC Asp	GCG Ala	G CTA	GAC Asp 285) Ası	TTC Phe	GAT Asp	864
50	CT(GA(1 As) 29(Met	TTC	GGG Gly	GAC Asp	GGG Gly 295	/ Asp	TCC Ser	CCC Pro	GGT Gly	r CCC y Pro 300	Gl3	A TT	r ACC	c ccc r Pro	912
55	CA(His	s As	C TCC p Set	C GCC	c ccc	TAC Ty:	Gly	C GCT / Ala	r CTO	G GAT 1 Asp	T ATO Met 31	t Ala	GA(C TT	C GAG	G TTT u Phe 320	960
	GA(G CA	G AT	G TT	r ACC	C GAS	CCO Pro	CT'	r GGA	A AT	r GA e As	C GAO	G TAG u Ty:	C GG r Gl	T GG y Gl	g TAG Y	1008

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

- 10 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1 5 10 15
 - Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 20 25 30
 - Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35 40 45
- Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 20 50 55 60
 - Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 65 70 75 80
- 25 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly 85 90 95
 - Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 100 105 110
 - Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 115 120 125
- Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 35 130 135 140
 - Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 145 150 155 160
- 40 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu 165 170 175
 - Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu 180 185 190
 - Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala 195 200 205
- Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly 210 215 220
 - Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala 225 230 235 240
- 55 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser

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Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp 265 260 5 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp 280 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro 295 10 290 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe 310 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly 15 330 325 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS: 20

(A) LENGTH: 894 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Herpes Simplex Virus
- (B) STRAIN: K12, KOS
- (C) INDIVIDUAL ISOLATE: tTA_S transactivator

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1..894

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 1..894

40 (ix) FEATURE:

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- (A) NAME/KEY: misc. binding
- (B) LOCATION: 1..207

(ix) FEATURE: 45

- (A) NAME/KEY: misc. binding
- (B) LOCATION: 208..297

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu 55

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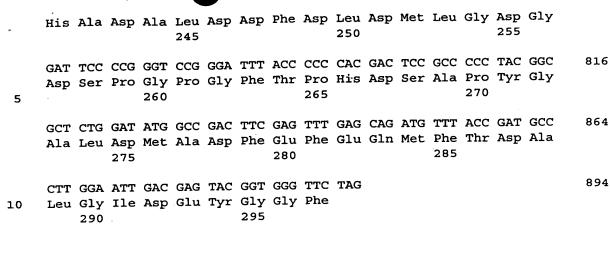
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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu 1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln 20 25 30

- 25 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys 35 40 45
 - Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His 50 55 60
 - Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg 65 70 75 80
- Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
 85 90 95
 - Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr 100 105 110
- 40 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu 115 120 125
 - Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys 130 135 140
 - Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr 145 150 155 160
- Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu 50 165 170 175

•	Phe	Asp	His	Gln 180	Gly	Ala	Glu	Pro	Ala 185	Phe	Leu	Phe	Gly	Leu 190	Glu	Leu		
5	Ile	Ile	Cys 195	Gly	Leu	Glu	Lys	Gln 200	Leu	Lys	Cys	Glu	Ser 205	Gly	Ser	Asp		
	Pro	Ser 210	Ile	His	Thr	Arg 215	Arg	Leu	Ser	Thr	Ala	Pro 220	Pro	Thr	Asp	Val		
10	Ser 225	Leu	Gly	Asp	Glu	Leu 230	His	Leu	Asp	Gly	Glu 235	Asp	Val	Ala	Met	Ala 240		
15	His	Ala	Asp	Ala	Leu 245	Asp	Asp	Phe	Asp	Leu 250	Asp	Met	Leu	Gly	Asp 255	Gly .		
	Asp	Ser	Pro	Gly 260	Pro	Gly	Phe	Thr	Pro 265	His	Asp	Ser	Ala	Pro 270	Tyr	Gly		
20	Ala	Leu	Asp 275	Met	Ala	Asp	Phe	Glu 280	Phe	Glu	Gln	Met	Phe 285	Thr	Asp	Ala	•	
25	Leu	Gly 290	Ile	Asp	Glu	Tyr	Gly 295	Gly	Phe									
	(2)	INF	ORMA'	TION	FOR	SEQ	ID I	NO : 5	:									
30			i) S	(B) (C)	LEN TYP STR	GTH: E: n ANDE	ACTE 450 ucle DNES Y: 1	base ic a S: d	e pa: cid oubl									
35				MOLE				NA (geno	mic)								
		(vi)		ORG	RINA	RCE: M: H K12			omeg	alov	irus						
40	٠	(ix)		NAM	•	Y: m		450								,	
		((xi)	SEQU	ENCE	DES	CRIP	TION	ı: SE	Q II	NO:	5:					·	
45	GA	ATTCC	CTCG	AGTI	TACC	AC T	CCCT	'ATCA	G TG	ATAG	AGAA	AAG	TGAA	AGT	CGAG	TTTACC		60
	ACT	rccci	TATC	AGTO	ATA	AG A	AAAG	TGAA	A GI	CGAG	TTTA	CCP	CTCC	CTA	TCAG	TGATAG		120
																GTCGAG		180
																TATCAG		240
																AGTGAAA		300
50	GT	CGAG	CTCG	GTAC	CCCG	GT (CGAGT	CAGGC	CG TO	TACC	3GTGC	GAC	:GCC	CATA	TAAC	CAGAGC		360

TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG	420
AAGACACCGG GACCGATCCA GCCTCCGCGG	450
(2) INFORMATION FOR SEQ ID NO:6:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	·
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:(A) ORGANISM: Human cytomegalovirus(B) STRAIN: Towne	
(ix) FEATURE: (A) NAME/KEY: mRNA (B) LOCATION: 382450	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
GAATTCCTCG ACCCGGGTAC CGAGCTCGAC TTTCACTTTT CTCTATCACT GATAGGGAGT	60
GGTAAACTCG ACTTTCACTT TTCTCTATCA CTGATAGGGA GTGGTAAACT CGACTTTCAC	120
TTTTCTCTAT CACTGATAGG GAGTGGTAAA CTCGACTTTC ACTTTTCTCT ATCACTGATA	180
GGGAGTGGTA AACTCGACTT TCACTTTTCT CTATCACTGA TAGGGAGTGG TAAACTCGAC	240
TTTCACTTTT CTCTATCACT GATAGGGAGT GGTAAACTCG ACTTTCACTT TTCTCTATCA	300
CTGATAGGGA GTGGTAAACT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC	360
TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG	420
AAGACACCGG GACCGATCCA GCCTCCGCGG	450
(2) INFORMATION FOR SEQ ID NO:7:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 398 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:(A) ORGANISM: Herpes Simplex Virus(B) STRAIN: KOS	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	

GAGCTCGACT TTCACTTTC TCTATCACTG ATAGGGAGTG GTAAACTCGA CTTTCACTTT

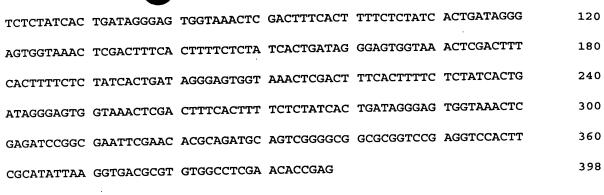
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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

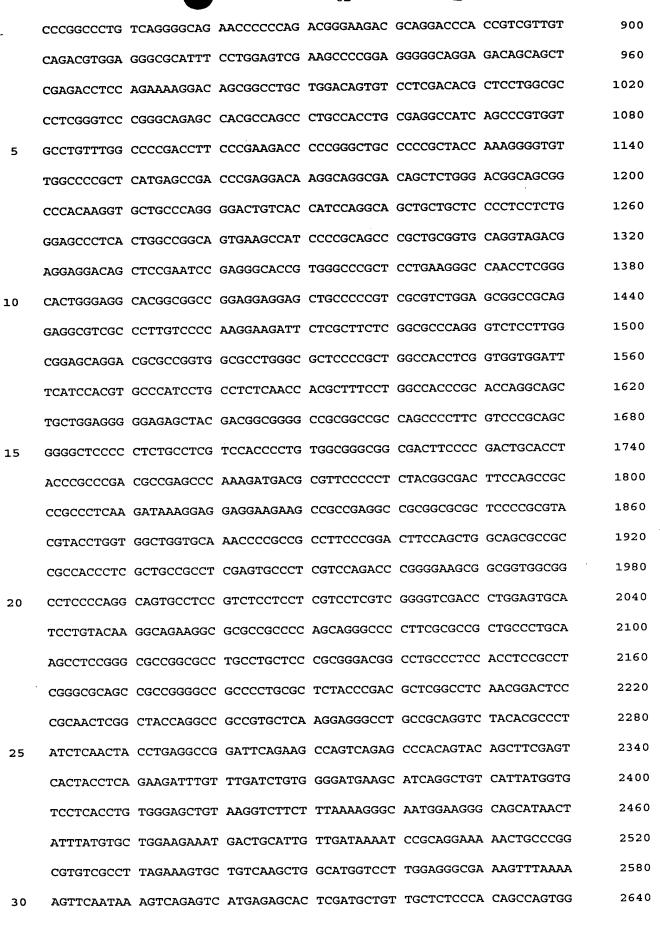
- (A) ORGANISM: Human cytomegalovirus
- (B) STRAIN: Towne (hCMV)

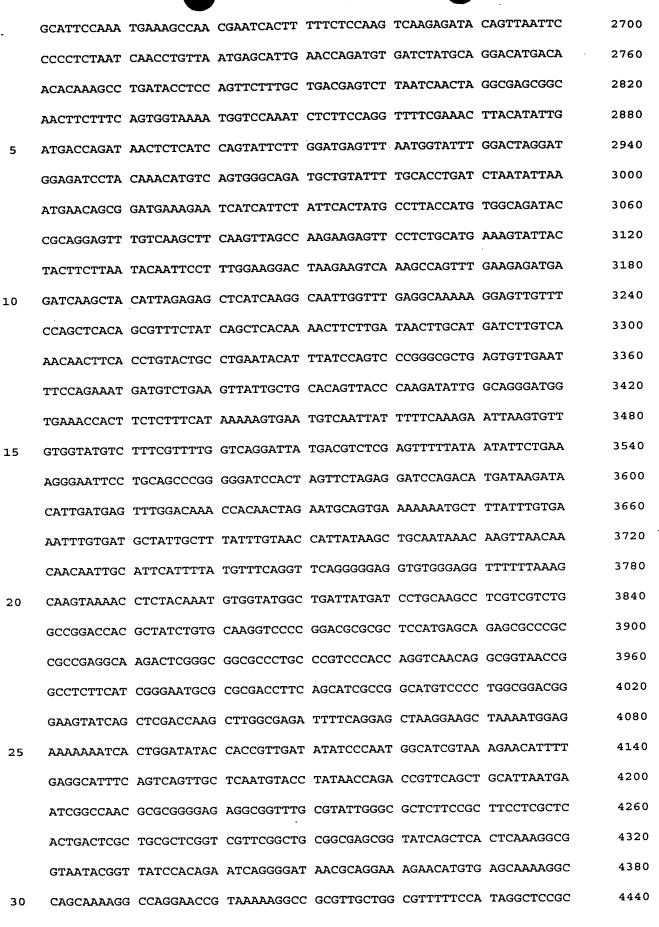
(vii) IMMEDIATE SOURCE:

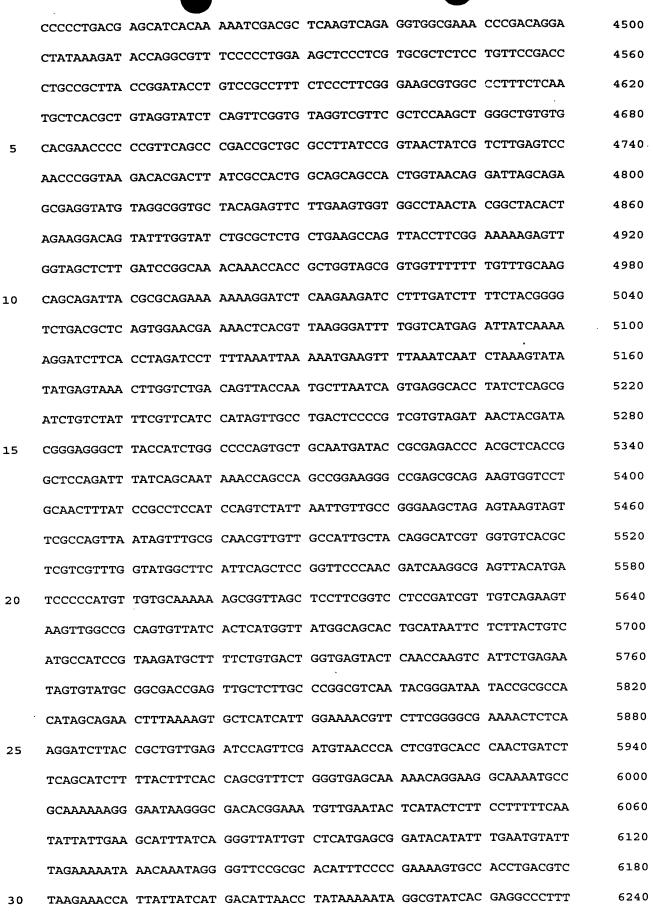
(B) CLONE: pUHD BGR3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCGAGTTTA CCACTCCCTA TCAGTGATAG AGAAAAGTGA AAGTCGAGTT TACCACTCCC 60 TATCAGTGAT AGAGAAAAGT GAAAGTCGAG TTTACCACTC CCTATCAGTG ATAGAGAAAA 120 GTGAAAGTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC 180 ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG 240 AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG 300 CTCGGTACCC GGGTCGAGTA GGCGTGTACG GTGGGAGGCC TATATAAGCA GAGCTCGTTT 360 AGTGAACCGT CAGATCGCCT GGAGACGCCA TCCACGCTGT TTTGACCTCC ATAGAAGACA 420 CCGGGACCGA TCCAGCCTCC GCGGCCCCGA ATTCGAGCTC GGTACCGGGC CCCCCTCGA 480 GGTCGACGGT ATCGATAAGC TTGATATCGA ATTCCAGGAG GTGGAGATCC GCGGGTCCAG 540 CCAAACCCCA CACCCATTTT CTCCTCCTC TGCCCCTATA TCCCGGCACC CCCTCCTCCT 600 AGCCCTTTCC CTCCTCCCGA GAGACGGGGG AGGAGAAAAG GGGAGTTCAG GTCGACATGA 660 CTGAGCTGAA GGCAAAGGAA CCTCGGGCTC CCCACGTGGC GGGCGGCGCG CCCTCCCCCA 720 CCGAGGTCGG ATCCCAGCTC CTGGGTCGCC CGGACCCTGG CCCCTTCCAG GGGAGCCAGA 780 CCTCAGAGGC CTCGTCTGTA GTCTCCGCCA TCCCCATCTC CCTGGACGGG TTGCTCTTCC 840







CGTC 62

(2) INFORMATION FOR SEQ ID NO:9:

151	CECTENCE	CHARACTERISTICS
(1)	SECUENCE	CHARACIERISIICS

- (A) LENGTH: 4963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Human cytomegalovirus

(vii) IMMEDIATE SOURCE:

(B) CLONE: pUHD BGR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCGAGTTTA CCACTCCCTA TCAGTGATAG AGAAAAGTGA AAGTCGAGTT TACCACTCCC 60 TATCAGTGAT AGAGAAAAGT GAAAGTCGAG TTTACCACTC CCTATCAGTG ATAGAGAAAA 120 GTGAAAGTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC 180 ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG 240 AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG 300 CTCGGTACCC GGGTCGAGTA GGCGTGTACG GTGGGAGGCC TATATAAGCA GAGCTCGTTT 360 AGTGAACCGT CAGATCGCCT GGAGACGCCA TCCACGCTGT TTTGACCTCC ATAGAAGACA 420 CCGGGACCGA TCCAGCCTCC GCGGCCCCGA ATTCCGGCCA CGACCATGAC CATGACCCTC 480 CACACCAAAG CATCTGGGAT GGCCCTACTG CATCAGATCC AAGGGAACGA GCTGGAGCCC 540 CTGAACCGTC CGCAGCTCAA GATCCCCCTG GAGCGGCCCC TGGGCGAGGT GTACCTGGAC 600 AGCAGCAAGC CCGCCGTGTA CAACTACCCC GAGGGCGCCG CCTACGAGTT CAACGCCGCG 660 GCCGCCGCCA ACGCGCAGGT CTACGGTCAG ACCGGCCTCC CCTACGGCCC CGGGTCTGAG 720 GCTGCGGCGT TCGGCTCCAA CGGCCTGGGG GGTTTCCCCC CACTCAACAG CGTGTCTCCG 780 AGCCCGCTGA TGCTACTGCA CCCGCCGCCG CAGCTGTCGC CTTTCCTGCA GCCCCACGGC 840 CAGCAGGTGC CCTACTACCT GGAGAACGAG CCCAGCGGCT ACACGGTGCG CGAGGCCGGC 900 CCGCCGGCAT TCTACAGGCC AAATTCAGAT AATCGACGCC AGGGTGGCAG AGAAAGATTG 960 GCCAGTACCA ATGACAAGGG AAGTATGGCT ATGGAATCTG CCAAGGAGAC TCGCTACTGT 1020 GCAGTGTGCA ATGACTATGC TTCAGGCTAC CATTATGGAG TCTGGTCCTG TGAGGGCTGC 1080 AAGGCCTTCT TCAAGAGAAG TATTCAAGGA CATAACGACT ATATGTGTCC AGCCACCAAC 1140 CAGTGCACCA TTGATAAAAA CAGGAGGAAG AGCTGCCAGG CCTGCCGGCT CCGCAAATGC 1200

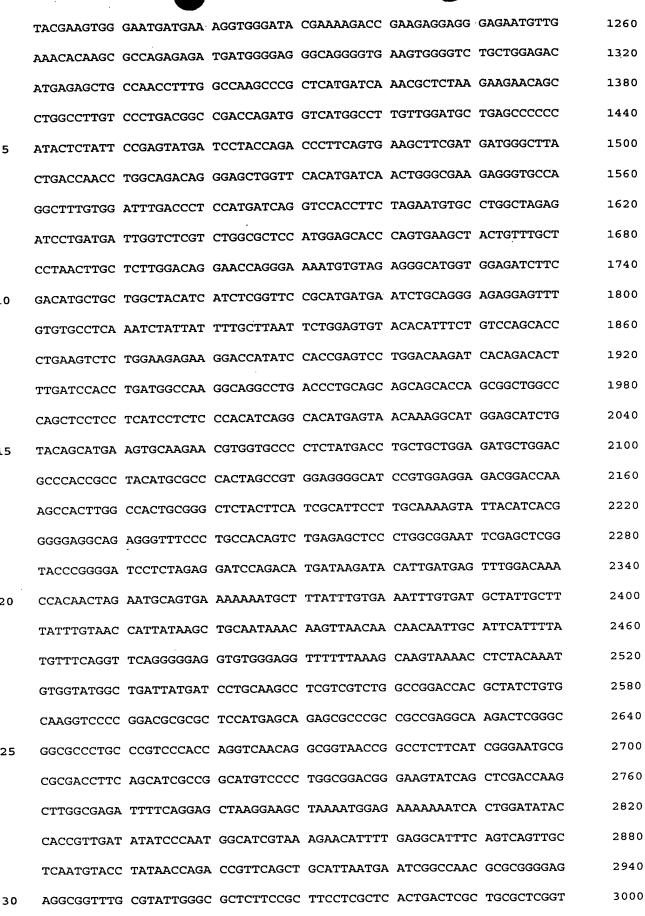
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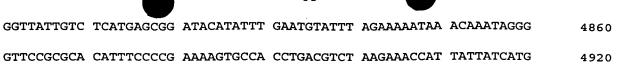
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5 (2) INFORMATION FOR SEQ ID NO:10:

1	ſi	١.	SECUENCE	CHARAC	TERTS	TTCS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

ACATTAACCT ATAAAAATAG GCGTATCACG AGGCCCTTTC GTC

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA AG

42